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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/451,527

DATE: 12/16/1999  
TIME: 16:05:39

Input Set: I451527.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Sim, Gek-Kee
2   Yang, Shumin
3   Dreitz, Matthew J.
4   Wonderling, Ramani S.
5 <120> TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
6   ACID MOLECULES, AND USES THEREOF
7 <130> FILE REFERENCE: IM-2-C2
8 <140> CURRENT APPLICATION NUMBER: US/09/451,527
9 <141> CURRENT FILING DATE: 1999-12-01
10 <150> EARLIER APPLICATION NUMBER: 09/322,409
11 <151> EARLIER FILING DATE: 1999-05-28
12 <150> EARLIER APPLICATION NUMBER: 60/087,306
13 <151> EARLIER FILING DATE: 1998-05-29
14 <160> NUMBER OF SEQ ID NOS: 174
15 <170> SOFTWARE: PatentIn Ver. 2.0
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17 <211> LENGTH: 549
18 <212> TYPE: DNA
19 <213> ORGANISM: Canis familiaris
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22 <222> LOCATION: (43)..(438)
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26                                     1
27   tcc caa ctg att cca act ctg gtc tgc tta cta gca ctc acc agc acc      102
28   Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala Leu Thr Ser Thr
29       5              10              15              20
30   ttt gtc cac gga cat aac ttc aat att act att aaa gag atc atc aaa      150
31   Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys
32               25              30              35
33   atg ttg aac atc ctc aca gcg aga aac gac tcg tgc atg gag ctg act      198
34   Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr
35               40              45              50
36   gtc aag gac gtc ttc act gct cca aag aac aca agc gat aag gaa atc      246
37   Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile
38       55              60              65
39   ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc      294
40   Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys
41       70              75              80
42   tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agc atg gca      342
43   Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala
44       85              90              95              100
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46      Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
47              105                      110                      115
48      ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat      438
49      Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
50              120                      125                      130
51      tgaagctgaa tattttaatt tatgagtttt taaatagctt tatttttaaaa atatttatat 498
52      atttataaca taataaaata aaatatatat agaaaaaaaa aaaaaaaaaa a      549
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54      <211> LENGTH: 132
55      <212> TYPE: PRT
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57      <400> SEQUENCE: 2
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60      Leu Thr Ser Thr Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys
61              20              25              30
62      Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys
63              35              40              45
64      Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
65              50              55              60
66      Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
67              65              70              75              80
68      Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
69              85              90              95
70      Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
71              100             105             110
72      Thr Leu Lys Asp Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys
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80      <400> SEQUENCE: 3
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83      gtatttcctt tgcattgatca ctttttagcct ttccaagaag tctttcagtg tactcttctt 180
84      gatttcattc atagaacagg tcttggtttgc catgctgctg aggttcctgt agagtcctct 240
85      gagatatctg ttggagcagt tgtgtgtata gatctgccgc agtacagtag cagctctgca 300
86      gaagatttcc ttatcgcttg tgttcttttg agcagtgaag acgtccttga cagtcagctc 360
87      catgcacgag tcgtttctcg ctgtgaggat gttcaacatt ttgatgatct ctttaatagt 420
88      aatattgaag ttatgtccgt ggacaaagggt gctggtgagt gctagtaagc agaccagagt 480
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93      <212> TYPE: DNA
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98 ctcacagcga gaaacgactc gtgcatggag ctgactgtca aggacgtctt cactgctcca 180  
99 aagaacacaa gcgataagga aatcttctgc agagctgcta ctgtactgcg gcagatctat 240  
100 acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300  
101 aacaagacct gttctatgaa tgaaatcaag aagagtacac tgaaagactt cttggaaagg 360  
102 ctaaaagtga tcatgcagaa gaaatactac aggcac 396

103 &lt;210&gt; SEQ ID NO 5

104 &lt;211&gt; LENGTH: 396

105 &lt;212&gt; TYPE: DNA

106 &lt;213&gt; ORGANISM: Canis familiaris

107 &lt;400&gt; SEQUENCE: 5

108 atgcctgtag tatttcttct gcatgatcac ttttagcctt tccaagaagt ctttcagtgt 60  
109 actcttcttg atttcattca tagaacaggt cttgtttgcc atgctgctga ggttcctgta 120  
110 gagtcctctg agatatctgt tggagcagtt gtgtgtatag atctgccgca gtacagtagc 180  
111 agctctgcag aagatttctt tatcgtctgt gttctttgga gcagtgaaga cgtccttgac 240  
112 agtcagctcc atgcacgagt cgtttctcgc tgtgaggatg ttcaacattt tgatgatctc 300  
113 tttaatatgta atattgaagt tatgtccgtg gacaaagggt ctggtgagtg ctagtaagca 360  
114 gaccagagtt ggaatcagtt gggaggtgag acccat 396

115 &lt;210&gt; SEQ ID NO 6

116 &lt;211&gt; LENGTH: 1013

117 &lt;212&gt; TYPE: DNA

118 &lt;213&gt; ORGANISM: Canis familiaris

119 &lt;220&gt; FEATURE:

120 &lt;221&gt; NAME/KEY: CDS

121 &lt;222&gt; LOCATION: (35)..(916)

122 &lt;400&gt; SEQUENCE: 6

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124 Met Ile Val Leu Ala Pro Ala  
125 1 5  
126 tgg agc cca act gcc tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc 103  
127 Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly  
128 10 15 20  
129 ctc cgc ggg acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc 151  
130 Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser  
131 25 30 35  
132 acc ttc gcg gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac 199  
133 Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp  
134 40 45 50 55  
135 tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg 247  
136 Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly  
137 60 65 70  
138 gcg ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag 295  
139 Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln  
140 75 80 85  
141 gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg 343  
142 Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr  
143 90 95 100  
144 gag ata cac ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt 391

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145      Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys
146          105                      110                      115
147      ctt cgc ttc gtc cag acc aac atc tcc cac ctg cag gac acc tcc      439
148      Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser
149          120                      125                      130                      135
150      cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc      487
151      Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser
152          140                      145                      150
153      ggg tgc ctg gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc      535
154      Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro
155          155                      160                      165
156      cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag      583
157      Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln
158          170                      175                      180
159      gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg      631
160      Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu
161          185                      190                      195
162      atg tcc act gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg      679
163      Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg
164          200                      205                      210                      215
165      tca ccc tac cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc      727
166      Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser
167          220                      225                      230
168      cat ctg ccc gag gac aca gag ctg gga cct gga ggg agt cag cta gag      775
169      His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu
170          235                      240                      245
171      act ggt ccc ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga      823
172      Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly
173          250                      255                      260
174      tca agg caa cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca      871
175      Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro
176          265                      270                      275
177      cct ctc ccc ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata      916
178      Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
179          280                      285                      290
180      taaatcatcc ttttctacca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 976
181      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa      1013
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184      <212> TYPE: PRT
185      <213> ORGANISM: Canis familiaris
186      <400> SEQUENCE: 7
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190          20                      25                      30
191      Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
192          35                      40                      45
193      Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
194          50                      55                      60

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/451,527

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195      Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
196      65                      70                      75                      80
197      Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
198                      85                      90                      95
199      Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
200                      100                     105                     110
201      Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
202                      115                     120                     125
203      His Leu Leu Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp
204                      130                     135                     140
205      Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
206      145                      150                      155                      160
207      Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala
208                      165                      170                      175
209      Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu
210                      180                      185                      190
211      Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp
212                      195                      200                      205
213      Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr
214                      210                      215                      220
215      Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly
216      225                      230                      235                      240
217      Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala
218                      245                      250                      255
219      Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro
220                      260                      265                      270
221      Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu
222                      275                      280                      285
223      Pro Pro Arg Asn Cys Ile
224                      290

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&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 1013

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Canis familiaris

&lt;400&gt; SEQUENCE: 8

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232      actttgtaca gagggggaga ggtggggctg gggctggctt tgggggcgtt gggggcgggc 180
233      gttgccttga tcctggggag ggagcagcgc gggctgcgtg gtcgaggaag ggaccagtct 240
234      ctagctgact ccctccaggt cccagctctg tgcctcggg cagatggctc cgctcgctgg 300
235      gcctcagtgt cctctgctcc ccagggtagg gtgacctccg ccgccgcctc cttecgcaat 360
236      gcaggcacca ggcagtggac atcagcagga gagccacggg cagcagcagc aggaggagca 420
237      gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccggg ctccttgggg 480
238      gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 540
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VERIFICATION SUMMARY  
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Original Text

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